

Replacement Page

ABSTRACT

The present invention is directed to a method for alignment of nucleic acid data traces. The method involves selecting reference alignment points from among internal peaks representing highly conserved bases, preferably consisting of heterogeneous multiplets. The alignment points may also optionally include the primer peak and/or the full-length peak. Reference position numbers are assigned to these alignment points reflecting the known relative position of the alignment point, a sequence position number is assigned to peaks in the data traces so as to maximize assigning the sequence position number and the reference position number to the same base. Optionally, the method may include the step of determining the average peak spacing interval between alignment points and assigning a sequence position number to peaks occurring at the intervals. The data traces are then aligned based on the assigned sequence position numbers.